This Raw Listing contains the General Information Section and up to the first 5 pages.

Does Not Comply
Corrected Diskette Needed

```
      1                          SEQUENCE LISTING
      2
      3  (1)    General Information:
      4
-->   5       (i) APPLICANT:
-->   6            (A) NAME: Burkly, Linda C.
-->   7            (B) STREET: 34 Winthrop Street
-->   8            (C) CITY: West Newton
-->   9            (D) STATE: Massachusetts
-->  10            (E) COUNTRY: USA
-->  11            (F) POSTAL CODE (ZIP): 02165
     12
-->  13            (A) NAME: Biogen, Inc.
-->  14            (B) STREET: Fourteen Cambridge Center
-->  15            (C) CITY: Cambridge
-->  16            (D) STATE: Massachusetts
-->  17            (E) COUNTRY: USA
-->  18            (F) POSTAL CODE (ZIP): 02142
     19
     20      (ii) TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES
     21
     22     (iii) NUMBER OF SEQUENCES: 15
     23
     24      (iv) COMPUTER READABLE FORM:
     25           (A) MEDIUM TYPE: Floppy disk
     26           (B) COMPUTER: IBM PC compatible
     27           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     28           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
     29
     30       (v) CURRENT APPLICATION DATA:
     31           (A) APPLICATION NUMBER: US 000000 (BGP-151CP)
     32           (B) FILING DATE:
     33      (vi) PRIOR APPLICATION DATA:
     34           (A) APPLICATION NUMBER: PCT/US94/01456
     35           (B) FILING DATE: 09-FEB-1994
     36     (vii) PRIOR APPLICATION DATA:
     37           (A) APPLICATION NUMBER: US 08/029,330
     38           (B) FILING DATE: 09-FEB-1993
     39
     40  (2) INFORMATION FOR SEQ ID NO: 1:
     41
     42       (i) SEQUENCE CHARACTERISTICS:
     43           (A) LENGTH: 360 base pairs
     44           (B) TYPE: nucleic acid
     45           (C) STRANDEDNESS: single
     46           (D) TOPOLOGY: linear
```

OK

Please see, also, back pages. Per 1.824 of Sequence Rules, the computer readable form shall contain a single file on which is recorded a printable copy of the Sequence Listing.

Delete (A) APPLICATION NUMBER: US 000000 (BGP-151CP) (B) FILING DATE: Leading

Please delete all TAB codes between amino acid numbers. They do not process well in the CRF program and cause misalignment. Use space characters instead.

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
 1               5                  10                  15

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
    ~~20~~      20          ~~25~~      25          ~~30~~      30

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
 35                  40                  45

Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
     50                  55                  60

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
 65                  70                  75                  80

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85                  90                  95

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
    100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser
115                 120
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..318
(D) OTHER INFORMATION:/product= "HP1/2 light chain variable region"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

--> **(A) LENGTH: 386 base pairs**

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

see next Page

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..386

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..57

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 58..386

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(D) OTHER INFORMATION:/note= "pBAG198 insert: VK2 (SVMDY) light chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT        48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-19             -15                 -10                 -5

GTC CAC TCC AGC ATC GTG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC        96
Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
      1               5                  10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG       144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
     15                  20                  25

ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG       192
Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 30                  35                  40                  45

CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA GAT AGA       240
Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
 50                  55                  60

TTC AGC GGT AGC GGT TAT GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC       288
```

INPUT SET: S15870.raw

```
378  Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
379       65                  70                  75
380
381  CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC      336
382  Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
383   80                  85                  90
384
385  TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG      384
386  Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
387       95                  100                 105
388
389  TG
390
391
```

386 ← move over from rt. margin

[56] Carlos et al., 1990, Blood 17:965, "Vascular Cell Adhesion molecule-1 (V

[57] Miller et al., 1993, J. Exp. Med. 178:211.

[58] L. Osborn et al., "Direct Expression Cloning of Vascular Cell Adhesion M

[59] J. Devlin et al., "Random Peptide Libraries: A Source of Specific Protei

[60] J. Scott and G. Smith, "Searching for Peptide Ligands with an Epitope Li

[61] U.S. Patent 4,833,092, Geysen, "Method For Determining Mimotopes", issue

The foregoing documents are incorporated herein by reference in their en

SEQUENCE LISTING

Sample of large amount of material preceding actual Sequence Listing. Please delete.

These appeared AFTER Sequence Listing. 08/447,118A
Please delete.

CLAIMS:

1. A method for the prevention of insulin dependent (type I) diabet

2. A method according to claim 1, wherein the anti-VLA-4 antibody s

3. A method according to claim 1, wherein the anti-VLA-4 antibody i

4. A method according to claim 1, wherein the anti-VLA-4 antibody i

Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the *Federal Register* (55 FR 18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

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   Cost: $25.00

For Further Information Contact: **Arti Shah at 703-308-4212**